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O I P E

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/023,601

DATE: 08/08/2002 P.6
TIME: 09:32:14

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3 <110> APPLICANT: Padigaru, Muralidhara
4 Kekuda, Ramesh
5 Colman, Steven
6 Spytek, Kimberly
7 Ballinger, Robert
8 Vernet, Corine
9 Li, Li
10 Shenoy, Suresh
11 Casman, Stacie
12 Guzev, Vladimir
14 <120> TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
16 <130> FILE REFERENCE: 21402-224AF
18 <140> CURRENT APPLICATION NUMBER: 10/023,601
19 <141> CURRENT FILING DATE: 2001-12-18
21 <150> PRIOR APPLICATION NUMBER: 60/256,635
22 <151> PRIOR FILING DATE: 2000-12-18
24 <150> PRIOR APPLICATION NUMBER: 60/259,743
25 <151> PRIOR FILING DATE: 2001-01-04
27 <150> PRIOR APPLICATION NUMBER: 60/299,327
28 <151> PRIOR FILING DATE: 2001-06-19
30 <150> PRIOR APPLICATION NUMBER: 60/261,498
31 <151> PRIOR FILING DATE: 2001-01-12
33 <150> PRIOR APPLICATION NUMBER: 60/263,689
34 <151> PRIOR FILING DATE: 2001-01-24
36 <150> PRIOR APPLICATION NUMBER: 60/267,464
37 <151> PRIOR FILING DATE: 2001-02-08
39 <150> PRIOR APPLICATION NUMBER: 60/271,021
40 <151> PRIOR FILING DATE: 2001-02-22
42 <150> PRIOR APPLICATION NUMBER: 60/275,946
43 <151> PRIOR FILING DATE: 2001-03-14
45 <150> PRIOR APPLICATION NUMBER: 60/278,150
46 <151> PRIOR FILING DATE: 2001-03-23
48 <150> PRIOR APPLICATION NUMBER: 60/285,718
49 <151> PRIOR FILING DATE: 2001-04-23
51 <150> PRIOR APPLICATION NUMBER: 60/312,902
52 <151> PRIOR FILING DATE: 2001-08-16
54 <150> PRIOR APPLICATION NUMBER: 60/257,876
55 <151> PRIOR FILING DATE: 2000-12-21
57 <150> PRIOR APPLICATION NUMBER: 60/260,718
58 <151> PRIOR FILING DATE: 2001-01-10
60 <150> PRIOR APPLICATION NUMBER: 60/284,591
61 <151> PRIOR FILING DATE: 2001-04-18
63 <160> NUMBER OF SEQ ID NOS: 102

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68 <211> LENGTH: 993

69 <212> TYPE: DNA

70 <213> ORGANISM: Homo sapiens

72 <400> SEQUENCE: 1

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75 gtaactggaa acttgggaat gattgtctct atccgaattg attcccgctt tcacacaccc 180
76 atgtactttt tctcagcca cctgtccttt gtggacacct gcttctcctc agttgtgagc 240
77 cccaagatgc tcaactgactt ctttgtgaag aggaaagcca tttctttcct tggctgtgct 300
78 ttgcagcagt ggttcttttg gttctttgtg gcagcagact gtttctctt ggagtccatg 360
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81 cacacaacaa atgcattttg tctccctttt tgtggcccta atgtcatcaa tcctttcttc 540
82 tgtgatatgt ccccttact ttccttgta tgtgctgata ccaggctcaa taagttggca 600
83 gttttcatcg tggtggagc tgtgggagtc ttcagtggc tgactatcct gatttcctac 660
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85 tctacttgct cttctcacct gacagctgtt ttcattctgt atgggtaccct tttctttatt 780
86 tatgtacatc ccagtgcac cttctccctg gatctcaata aagtagtgct tgtgttttac 840
87 acagcagtga ttcctatgtt gaaccactt atctacagct tgagaaacaa ggaagtcaaa 900
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93 <211> LENGTH: 314

94 <212> TYPE: PRT

95 <213> ORGANISM: Homo sapiens

97 <400> SEQUENCE: 2

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102           20           25           30
104 Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
105           35           40           45
107 Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
108           50           55           60
110 Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
111  65           70           75           80
113 Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
114           85           90           95
116 Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
117           100          105          110
119 Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
120           115          120          125
122 Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
123           130          135          140
125 Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
126 145          150          155          160
128 Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn

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131 Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
132          180          185          190
134 Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
135          195          200          205
137 Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
138          210          215          220
140 Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
141 225          230          235          240
143 Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr Leu
144          245          250          255
146 Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
147          260          265          270
149 Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
150          275          280          285
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167 gtaactggaa acttgggaat gattgtcctc atccgaattg attcccgcct tcacacaccc 180
168 atgtactttt tcctcagcca cctgtccttt gtggacacct gcttctcctc agttgtgagc 240
169 cccaagatgc tcaactgactt ctttgtgaag aggaaagcca tttctttcct tggctgtgct 300
170 ttgcagcagt ggttcttttg gttctttgtg gcagcagact gtttctctt ggagtccatg 360
171 gcctatgact gctatgtggc catctgtaac ccattgttat actcagttgc tatgtcccag 420
172 aggcctctgca tccagctagt ggtgggtccc tatgtcattg gactcatgaa taccatgact 480
173 cacacaacaa atgcattttg tctccctttt tgtggcccta atgtcatcaa tcctttcttc 540
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178 tatgtacatc ccagtgaac cttctccctg gatctcaata aagtagtgct tgtgttttac 840
179 acagcagtga ttctatgtt gaaccactt atctacagct tgagaaacaa ggaagtcaaa 900
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186 <212> TYPE: PRT
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193 Leu Asn Tyr Asn Pro Gln Leu Gln Val Phe Leu Phe Leu Leu Phe Leu

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196 Thr Thr Phe Tyr Val Ile Asn Val Thr Gly Asn Leu Gly Met Ile Val
197          35          40          45
199 Leu Ile Arg Ile Asp Ser Arg Leu His Thr Pro Met Tyr Phe Phe Leu
200          50          55          60
202 Ser His Leu Ser Phe Val Asp Thr Cys Phe Ser Ser Val Val Ser Pro
203 65          70          75          80
205 Lys Met Leu Thr Asp Phe Phe Val Lys Arg Lys Ala Ile Ser Phe Leu
206          85          90          95
208 Gly Cys Ala Leu Gln Gln Trp Phe Phe Gly Phe Phe Val Ala Ala Asp
209          100          105          110
211 Cys Phe Leu Leu Glu Ser Met Ala Tyr Asp Cys Tyr Val Ala Ile Cys
212          115          120          125
214 Asn Pro Leu Leu Tyr Ser Val Ala Met Ser Gln Arg Leu Cys Ile Gln
215          130          135          140
217 Leu Val Val Gly Pro Tyr Val Ile Gly Leu Met Asn Thr Met Thr His
218 145          150          155          160
220 Thr Thr Asn Ala Phe Cys Leu Pro Phe Cys Gly Pro Asn Val Ile Asn
221          165          170          175
223 Pro Phe Phe Cys Asp Met Ser Pro Leu Leu Ser Leu Val Cys Ala Asp
224          180          185          190
226 Thr Arg Leu Asn Lys Leu Ala Val Phe Ile Val Ala Gly Ala Val Gly
227          195          200          205
229 Val Phe Ser Gly Leu Thr Ile Leu Ile Ser Tyr Ile Tyr Ile Leu Met
230          210          215          220
232 Ala Ile Leu Arg Ile Arg Ser Ala Asp Gly Arg Cys Lys Thr Phe Ser
233 225          230          235          240
235 Thr Cys Ser Ser His Leu Thr Ala Val Phe Ile Ser Tyr Gly Thr Leu
236          245          250          255
238 Phe Phe Ile Tyr Val His Pro Ser Ala Thr Phe Ser Leu Asp Leu Asn
239          260          265          270
241 Lys Val Val Ser Val Phe Tyr Thr Ala Val Ile Pro Met Leu Asn Pro
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259 aatatcgga tgatgttggt aatcaaggtc agtcctcagc ttaacagccc catgtacttt 180
260 ttccctcagtc acttgctcatt tgttgatgtg tggttttctt ccaatgtcac ccctaaaatg 240
261 ttggaaaatc tgttatcaga taaaaaaca atttcttatg ctggctgttt agcacagtgt 300
262 ttcttcttca ttgctcttgt ccatgtggaa atttttattc ttgctgcgat tgcctttgat 360
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265 tggacttatg gcttgtaactt ctgtggaaaa attgagatca accatttcta ctgtgcagat 540
266 ccacctctca tcaaaatggc ctgtgccggg acctttgtaa aagaatatac aatgctcata 600
267 cttgccggca tcaacttcac atattccctg actgtaatta tcattcttta cttattcatc 660
268 ctcatcgcca ttctgcgaat gcgctcagca gaaggaaggc agaaggcctt ttccacatgt 720
269 ggggtcccatc tgacagctgt catcatattc tatggtactc tgatcttcat gtatctcaga 780
270 cgtcccacag aggagtctgt ggagcagggg aagatggtgg ctgtgttcta taccacagtg 840
271 atcccatgt tgaatcccat gatctacagt ctgaggaaca aggatgtgaa aaaggccatg 900
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276 <211> LENGTH: 307
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284 Ser Arg Arg Glu Trp Gln Val Leu Phe Phe Ile Val Phe Leu Val Val
285 20 25 30
287 Tyr Ile Ile Thr Val Val Gly Asn Ile Gly Met Met Leu Leu Ile Lys
288 35 40 45
290 Val Ser Pro Gln Leu Asn Ser Pro Met Tyr Phe Phe Leu Ser His Leu
291 50 55 60
293 Ser Phe Val Asp Val Trp Phe Ser Ser Asn Val Thr Pro Lys Met Leu
294 65 70 75 80
296 Glu Asn Leu Leu Ser Asp Lys Lys Thr Ile Ser Tyr Ala Gly Cys Leu
297 85 90 95
299 Ala Gln Cys Phe Phe Phe Ile Ala Leu Val His Val Glu Ile Phe Ile
300 100 105 110
302 Leu Ala Ala Ile Ala Phe Asp Arg Tyr Thr Val Ile Gly Asn Pro Leu
303 115 120 125
305 Leu Tyr Gly Ser Lys Met Ser Arg Asp Val Cys Ile Arg Leu Ile Thr
306 130 135 140
308 Phe Pro Tyr Ile Tyr Gly Phe Leu Thr Ser Leu Thr Ala Thr Leu Trp
309 145 150 155 160
311 Thr Tyr Gly Leu Tyr Phe Cys Gly Lys Ile Glu Ile Asn His Phe Tyr
312 165 170 175
314 Cys Ala Asp Pro Pro Leu Ile Lys Met Ala Cys Ala Gly Thr Phe Val
315 180 185 190
317 Lys Glu Tyr Thr Met Leu Ile Leu Ala Gly Ile Asn Phe Thr Tyr Ser
318 195 200 205
320 Leu Thr Val Ile Ile Ile Ser Tyr Leu Phe Ile Leu Ile Ala Ile Leu
321 210 215 220
323 Arg Met Arg Ser Ala Glu Gly Arg Gln Lys Ala Phe Ser Thr Cys Gly
324 225 230 235 240
326 Ser His Leu Thr Ala Val Ile Ile Phe Tyr Gly Thr Leu Ile Phe Met
327 245 250 255
329 Tyr Leu Arg Arg Pro Thr Glu Glu Ser Val Glu Gln Gly Lys Met Val
330 260 265 270
332 Ala Val Phe Tyr Thr Thr Val Ile Pro Met Leu Asn Pro Met Ile Tyr

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/023,601

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Input Set : A:\Cur524a1.app
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 9

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/023,601

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Input Set : A:\Cur524a1.app

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L:531 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0